

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hu, Sylvia
- (ii) TITLE OF INVENTION: Truncated Glial Cell Line-Derived
Neurotrophic Factor
- (iii) NUMBER OF SEQUENCES: 50
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: AMGEN INC.
(B) STREET: 1840 DeHavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: United States of America
(F) ZIP: 91320
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent In Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Curry, Daniel R.
(B) REGISTRATION NUMBER: 32,727
(C) REFERENCE/DOCKET NUMBER: A-357
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 805-447-8102
(B) TELEFAX: 805-499-8011
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..402

SUB B?

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCA CCA GAT AAA CAA ATG GCA GTG CTT CCT AGA AGA GAG CGG AAT CGG	48
Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg	
1 5 10 15	
CAG GCT GCA GCT GCC AAC CCA GAG AAT TCC AGA GGA AAA GGT CGG AGA	96
Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg	
20 25 30	
GGC CAG AGG GGC AAA AAC CGG GGT TGT GTC TTA ACT GCA ATA CAT TTA	144
Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu	
35 40 45	
AAT GTC ACT GAC TTG GGT CTG GGC TAT GAA ACC AAG GAG GAA CTG ATT	192
Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile	
50 55 60	
TTT AGG TAC TGC AGC GGC TCT TGC GAT GCA GCT GAG ACA ACG TAC GAC	240
Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp	
65 70 75 80	
AAA ATA TTG AAA AAC TTA TCC AGA AAT AGA AGG CTG GTG AGT GAC AAA	288
Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys	
85 90 95	
GTA GGG CAG GCA TGT TGC AGA CCC ATC GCC TTT GAT GAT GAC CTG TCG	336
Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser	
100 105 110	
TTT TTA GAT GAT AAC CTG GTT TAC CAT ATT CTA AGA AAG CAT TCC GCT	384
Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala	
115 120 125	
AAA AGG TGT GGA TGT ATC	402
Lys Arg Cys Gly Cys Ile	
130	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg	
1 5 10 15	
Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg	
20 25 30	
Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu	
35 40 45	

Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
50 55 60
Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
65 70 75 80
Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
85 90 95
Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
100 105 110
Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
115 120 125
Lys Arg Cys Gly Cys Ile
130

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys Asn Arg Gly
1

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Lys Asn Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Gly Lys Asn Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln Arg Gly Lys Asn Arg Gly
1 5

(2) INFORMATION FOR SEQ /ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gln Arg Gly Lys Asn Arg Gly
1 5

(2) INFORMATION/ FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg/Gly Gln Arg Gly Lys Asn Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg
1 5 10 15
Gly

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn
1 5 10 15
Arg Gly

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys
1 5 10 15
Asn Arg Gly

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly
 1 5 10 15

Lys Asn Arg Gly
 20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
 1 5 10 15

Gly Lys Asn Arg Gly
 20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln
 1 5 10 15

Arg Gly Lys Asn Arg Gly
 20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly
 1 5 10 15

Gln Arg Gly Lys Asn Arg Gly
 20

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 1 5 10 15

Gly Gln Arg Gly Lys Asn Arg Gly
 20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg
 1 5 10 15

Arg Gly Gln Arg Gly Lys Asn Arg Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
20 25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Arg Arg Gly Gln Arg Gly / Lys Asn Arg Gly
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
20 25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg
1 5 10 15

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

The first of these is the fact that the
 C_{60} molecule is a truncated icosahedron,
 which is a polyhedron with 32 faces, 60
 vertices, and 90 edges. The second is
 the fact that the C_{60} molecule is a
 highly symmetric molecule, with a
 symmetry group of I_h . The third is
 the fact that the C_{60} molecule is a
 highly stable molecule, with a
 dissociation energy of approximately
 10 eV per molecule.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID/NO:29:

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu
1 5 10 15

Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
 20 25 30

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro
 1 5 10 15
 Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg
 20 25 30
 Gly

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn
 1 5 10 15
 Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn
 20 25 30
 Arg Gly

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

(2) INFORMATION FOR SEQ ID NO:35:

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

(2) INFORMATION FOR SEQ /ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE / DESCRIPTION: SEQ ID NO:36:

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids

(The following are the names of the persons who have been appointed as members of the Board of Directors of the National Association of Manufacturers since the last meeting of the Board.)

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala
 1 5 10 15
 Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln
 20 25 30
 Arg Gly Lys Asn Arg Gly
 35

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln
 1 5 10 15
 Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly
 20 25 30
 Gln Arg Gly Lys Asn Arg Gly
 35

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CATATGTCTC CCGATAAACA AATGGCTGTT CTTCCACGTC GTGAACGTAA CCGTCAGGCG 60
 GCCGCTGCTA ACCCGGAGAA TTCCCGTGGT AAAGGTCGTC GTGGTCAGCG TGGTAAAAAC 120
 CGCGGTTGCG TTCTGACCGC TATCCACCTG AACGTTACCG ACCTGGGTCT CGGTTACGAA 180
 ACCAAAGAAG AATTAATCTT CCGTTACTGC TCCGGTTCCT GCGACGCTGC TGAAACCACG 240

TACGACAAAA TCCTGAAAAA CCTGTCCCGT AACCGTCGTC TGGTTTCCGA CAAAGTTGGT 300
 CAAGCTTGCT GCCGTCCGAT CGCTTTCGAC GACGACCTGT CTTTCCTGGA CGACAACCTG 360
 GTTTACCACA TCCTGCGTAA AACTCCGCT AAGCGTTGCG GTTGCATCTA AGGATCC 417

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CATATGAGCC CGGACAAACA GATGGCAGTA CTTCCACGTC GTGAACGTAA TCGCCAGGCA 60
 GCAGCTGCAA ACCCGGAAAA CTCCCGTGGT AAAGGTCGCC GTGGCCAGCG CGGCAAAAAC 120
 CGTGGTTGTG TTCTGACTGC AATCCACCTG AACGTTACTG ACCTGGGTCT GGGCTACGAA 180
 ACCAAAGAAG AACTGATCTT CCGCTACTGC AGCGGCTCTT GCGACGCAGC TGAAACCACT 240
 TACGACAAAA TCCTGAAAAA CCTGTCCCGT AACCGCCGTC TGGTAAGCGA CAAAGTAGGT 300
 CAGGCATGCT GCCGTCCGAT CGCATTCGAC GATGACCTGA GCTTCCTGGA TGACAACCTG 360
 GTTTACCACA TCCTGCGTAA AACTCCGCT AAACGCTGCG GTTGCATCTA AGGATCC 417

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATG TCC CCA GAA AAT TCT CGT GGT AAA GGT CGT CGT GGT CAG CGT GGT 48
 Met Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly
 135 140 145 150
 AAT AAC CGC GGT TGC GTT CTG ACC GCT ATC CAC CTG AAC GTT ACC GAC 96
 Asn Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp
 155 160 165

[illegible]

```

y Tyr Glu Thr Lys Glu Glu Leu Ile Ph
0 175

C GAC GCT GCT GAA ACC ACG TAC GAC AA
s Asp Ala Ala Glu Thr Thr Tyr Asp Ly
190 19

T AAC CGT CGT CTG GTT TCC GAC AAA GT
g Asn Arg Arg Leu Val Ser Asp Lys Va
205 210

G ATC GCT TTC GAC GAC GAC CTG TCC TT
o Ile Ala Phe Asp Asp Asp Leu Ser Ph
220 225

C CAC ATC CTG CGT AAA CAC TCC GCT AA
r His Ile Leu Arg Lys His Ser Ala Ly
235 240

N FOR SEQ ID NO:42:

UENCE CHARACTERISTICS:
A) LENGTH: 114 amino acids
B) TYPE: amino acid
D) TOPOLOGY: linear

ECULE TYPE: protein

UENCE DESCRIPTION: SEQ ID NO:42:

u Asn Ser Arg Gly Lys Gly Arg Arg Gl
5 10

y Cys Val Leu Thr Ala Ile His Leu As
0 25

y Tyr Glu Thr Lys Glu Glu Leu Ile Ph
40 4

s Asp Ala Ala Glu Thr Thr Tyr Asp Ly
55 60

g Asn Arg Arg Leu Val Ser Asp Lys Va
70 75

o Ile Ala Phe Asp Asp Asp Leu Ser Ph
85 90

r His Ile Leu Arg Lys His Ser Ala Ly
0 105

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: / SEQ ID NO:42:

[illegible]

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATG CGT GGT CAA CGT GGT AAA AAC CGC GGT TGC GTT CTG ACT GCA ATC	48
Met Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile	
115 120 125 130	
CAC CTG AAC GTT ACT GAC CTG GGT CTG GGC TAC GAA ACC AAA GAA GAA	96
His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu	
135 140 145	
CTG ATC TTC CGC TAC TGC AGC GGC TCT TGC GAC GCA GCT GAA ACC ACT	144
Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr	
150 155 160	
TAC GAC AAA ATC CTG AAA AAC CTG TCC CGT AAC CGC CGT CTG GTA AGC	192
Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser	
165 170 175	
GAC AAA GTA GGT CAG GCA TGC TGC CGT CCG ATC GCA TTC GAC GAT GAC	240
Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp	
180 185 190	
CTG AGC TTC CTG GAT GAC AAC CTG GTT TAC CAC ATC CTG CGT AAA CAC	288
Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His	
195 200 205 210	
TCC GCT AAA CGC TGC GGT TGC ATC TAA	315
Ser Ala Lys Arg Cys Gly Cys Ile	
215	

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile
1 5 10 15

- 78 -

(2) INFORMATION FOR SEQ ID NO:45:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATG	GGT	CAA	CGT	GGT	AAA	AAC	CGT	GGT	TGT	GTT	CTG	ACT	GCA	ATC	CAC	48
Met	Gly	Gln	Arg	Gly	Lys	Asn	Arg	Gly	Cys	Val	Leu	Thr	Ala	Ile	His	
105					110					115					120	
CTG	AAC	GTT	ACT	GAC	CTG	GGT	CTG	GGC	TAC	GAA	ACC	AAA	GAA	GAA	CTG	96
Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	
				125					130					135		
ATC	TTC	CGC	TAC	TGC	AGC	GGC	TCT	TGC	GAC	GCA	GCT	GAA	ACC	ACT	TAC	144
Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys	Asp	Ala	Ala	Glu	Thr	Thr	Tyr	
			140					145					150			
GAC	AAA	ATC	CTG	AAA	AAC	CTG	TCC	CGT	AAC	CGC	CGT	CTG	GTA	AGC	GAC	192
Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg	Asn	Arg	Arg	Leu	Val	Ser	Asp	
		155					160					165				
AAA	GTA	GGT	CAG	GCA	TGC	TGC	CGT	CCG	ATC	GCA	TTC	GAC	GAT	GAC	CTG	240
Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro	Ile	Ala	Phe	Asp	Asp	Asp	Leu	
	170					175					180					
AGC	TTC	CTG	GAT	GAC	AAC	CTG	GTT	TAC	CAC	ATC	CTG	CGT	AAA	CAC	TCC	288
Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	
185					190					195					200	

A-357

- 79 -

GCT AAA CGC TGC GGT TGC ATC TAA
Ala Lys Arg Cys Gly Cys Ile
205

312

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His
1 5 10 15
Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
20 25 30
Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
35 40 45
Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp
50 55 60
Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
65 70 75 80
Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser
85 90 95
Ala Lys Arg Cys Gly Cys Ile
100

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn
1 5 10 15
Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg
20 25 30
Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His
35 40 45

Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
 50 55 60
 Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
 65 70 75 80
 Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp
 85 90 95
 Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
 100 105 110
 Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser
 115 120 125
 Ala Lys Arg Cys Gly Cys Ile
 130 135

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile
 1 5 10 15
 His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu
 20 25 30
 Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr
 35 40 45
 Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser
 50 55 60
 Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp
 65 70 75 80
 Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His
 85 90 95
 Ser Ala Lys Arg Cys Gly Cys Ile
 100

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His
 1 5 10 15
 Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
 20 25 30
 Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
 35 40 45
 Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp
 50 55 60
 Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
 65 70 75 80
 Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser
 85 90 95
 Ala Lys Arg Cys Gly Cys Ile
 100

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly
 1 5 10 15
 Asn Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp
 20 25 30
 Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys
 35 40 45
 Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys
 50 55 60
 Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala
 65 70 75 80
 Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp
 85 90 95

A-357

- 82 -

Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly
100 105 110

Cys Ile

Sub
B2
(cont.)